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Sequence Listing could not be accepted due to errors.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: markspencer

Timestamp: [year=2009; month=6; day=19; hr=14; min=3; sec=41; ms=93;]

Reviewer Comments:

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E321 No. of Bases conflict, this line has no nucleotides

SEQID (10) POS (96)

E355 Empty lines found between the amino acid numbering and the proteins SEQID (10)

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Glu Ile Leu Met Thr Gln Ser Pro Ala Thr Leu Ser Val Ser Pro Gly

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Glu Arg Val Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Asn
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
35 40 45

Tyr Gly Ala Ser Thr Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Asn Ser Leu Gln Ser

70 75 80

Glu Asp Phe Ala Leu Tyr Tyr Cys His Glu Tyr Asn Gly Trp Pro Pro 85 90 95

Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr 100 105 110

2

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The Sequence Listing file must end at the bottom of the last SEQ ID #. There can be no extra information following the last SEQ ID # in the file. Please remove the extra information, "2" and "1", found at the end of the file, after SEQ ID # 10.

Validated By CRFValidator v 1.0.3

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     Kimura, Tsuyoshi
      Imaizumi, Atsuchi
      Takedo, Tae
      Co, May Sung
      Vasquez, Maximiliano
      TEIJIN LIMITED
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<140> 09700851
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gtc cag tgt gaa gtg cag ctg gtg gag tcg ggg gga ggc tta gtg aag
Val Gln Cys Glu Val Gln Leu Val Glu Ser Gly Gly Leu Val Lys
             20
cct gga ggg ccc ctg aaa ctc tcc tgt gca gcc tct gga ttc act ttc
Pro Gly Gly Pro Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
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                             40
                                                 45
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Ser Ser Tyr Gly Met Ser Trp Val Arg Gln Thr Pro Glu Lys Arg Leu

50 55 60

Glu Trp Val Ala Thr Ile Ser Thr Gly Gly Ser Tyr Thr Tyr Pro 70 75 gac agt gtg aag ggt cga ttc acc atc tcc aga gac aat gcc aag aac 288 Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn gcc ctg tat ctg caa atg agc agt ctg agg tct gag gac acg gcc ata 336 Ala Leu Tyr Leu Gln Met Ser Ser Leu Arg Ser Glu Asp Thr Ala Ile 100 105 tat tac tgt gca aga cgg ggg gac gca tgg ggt aac ttg gac tac tgg Tyr Tyr Cys Ala Arg Arg Gly Asp Ala Trp Gly Asn Leu Asp Tyr Trp 115 120 414 ggt caa gga acc tct gtc acc gtc tcc tca Gly Gln Gly Thr Ser Val Thr Val Ser Ser 130 135 <210> 2 <211> 138 <212> PRT <213> Mus musculus <220> <223> Figure 1(A): Heavy chain variable region of mouse antibody VTm1.1 (MuVTm1.1). <400> 2 Met Asn Phe Val Leu Ser Ser Ile Phe Leu Ala Leu Ile Leu Lys Gly 10 Val Gln Cys Glu Val Gln Leu Val Glu Ser Gly Gly Leu Val Lys 20 25 Pro Gly Gly Pro Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe 35 40 Ser Ser Tyr Gly Met Ser Trp Val Arg Gln Thr Pro Glu Lys Arg Leu 50 55 Glu Trp Val Ala Thr Ile Ser Thr Gly Gly Ser Tyr Thr Tyr Tyr Pro 65 70 75 Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn 90 Ala Leu Tyr Leu Gln Met Ser Ser Leu Arg Ser Glu Asp Thr Ala Ile 100 105 Tyr Tyr Cys Ala Arg Arg Gly Asp Ala Trp Gly Asn Leu Asp Tyr Trp

115 120 125

<210> 3 <211> 381 <212> DNA <213> Mus musculus <220> <221> CDS <222> (1)..(381) <220> <223> Figure 1(B): Light chain variable region of mouse VTm1.1 antibody (MuVTm1.1). atg gtt ttc aca cct cag ata ctt gga ctt atg ctt ttt tgg att tca 48 Met Val Phe Thr Pro Gln Ile Leu Gly Leu Met Leu Phe Trp Ile Ser 10 gcc tcc aga ggt gat gtt gtg cta act cag tct cca gcc acc ctg tct 96 Ala Ser Arg Gly Asp Val Val Leu Thr Gln Ser Pro Ala Thr Leu Ser 2.0 2.5 gtg act cca gga gat agc gtc agt ctt tcc tgc agg gcc agt caa act 144 Val Thr Pro Gly Asp Ser Val Ser Leu Ser Cys Arg Ala Ser Gln Thr att agc aac aac cta cac tgg tat caa cac aaa tca cat gag tct cca 192 Ile Ser Asn Asn Leu His Trp Tyr Gln His Lys Ser His Glu Ser Pro 50 55 60 agg ctt ctc atc aag tct gct tcc cag tcc atc tct ggg atc ccc tcc Arg Leu Leu Ile Lys Ser Ala Ser Gln Ser Ile Ser Gly Ile Pro Ser 65 70 75 agg ttc agt ggc agt gga tca ggg aca gat ttc act ctc agt atc aac 288 Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Ser Ile Asn 90 85 agt gtg gaa act gaa gat ttt gga atg tat ttc tgt caa cag agt tac Ser Val Glu Thr Glu Asp Phe Gly Met Tyr Phe Cys Gln Gln Ser Tyr 100 age tgg eeg ete aeg tte ggt get ggg ace aag etg gag etg aaa 381 Ser Trp Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys 115 120

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     VTml.1 antibody (MuVTml.1).
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Ala Ser Arg Gly Asp Val Val Leu Thr Gln Ser Pro Ala Thr Leu Ser
            20
                                25
Val Thr Pro Gly Asp Ser Val Ser Leu Ser Cys Arg Ala Ser Gln Thr
                           40
Ile Ser Asn Asn Leu His Trp Tyr Gln His Lys Ser His Glu Ser Pro
     50
                       55
Arg Leu Leu Ile Lys Ser Ala Ser Gln Ser Ile Ser Gly Ile Pro Ser
Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Ser Ile Asn
                85
                                     90
Ser Val Glu Thr Glu Asp Phe Gly Met Tyr Phe Cys Gln Gln Ser Tyr
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Ser Trp Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
      115
                          120
                                               125
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     humanized VTm1.1 antibody (HuVTm1.1).
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Met Asn Phe Val Leu Ser Ser Ile Phe Leu Ala Leu Ile Leu Lys Gly
1 5 10

gtc cag tgt gaa gtg caa ctg gtg gag tcg ggg gga ggc tta gtg cag 96 Val Gln Cys Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln 20 25 30

cct gga ggg tcc ctg aga ctc tcc tgt gca gcc tct gga ttc act ttc 144 Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe 35 40 45

_	agt Ser 50			_			_	_	_	_	_		_		_	192
	tgg Trp	-	_			_				_						240
_	agt Ser		_		_					_	_			_		288
	ctg Leu		_		_		_	_		_		_	_	_	_	336
	tac Tyr	_	_	_			_	_					Ī			384
	caa Gln 130				_		_									414
<212 <213 <220	1> 13 2> PE 3> Mu 0> 3> F:	RT us mu igure	e 2(<i>I</i>	A): I	Heav <u>y</u>	•				_	ion d	of				
<400	0> 6															
Met 1	Asn	Phe	Val	Leu 5	Ser	Ser	Ile	Phe	Leu 10	Ala	Leu	Ile	Leu	Lys 15	Gly	
Val	Gln	Cys	Glu 20	Val	Gln	Leu	Val	Glu 25	Ser	Gly	Gly	Gly	Leu 30	Val	Gln	
Pro	Gly	Gly 35	Ser	Leu	Arg	Leu	Ser 40	Суз	Ala	Ala	Ser	Gly 45	Phe	Thr	Phe	
Ser																
	Ser 50	Tyr	Gly	Met	Ser	Trp 55	Val	Arg	Gln	Ala	Pro 60	Gly	Lys	Gly	Leu	
Glu 65						55					60					
65	50	Val	Ala	Thr	Ile 70	55 Ser	Thr	Gly	Gly	Ser 75	60 Tyr	Thr	Tyr	Tyr	Pro 80	

Tyr Tyr Cys Ala Arg Arg Gly Asp Ala Trp Gly Asn Leu Asp Tyr Trp

115 120 125

Gly Gln Gly Thr Leu Val Thr Val Ser Ser 130 135

<210> 7 <211> 381 <212> DNA <213> Mus musculus <220> <221> CDS <222> (1)..(381) <220> <223> igure 2(B): Light chain variable region of humanized VTm1.1 antibody (HuVTm1.1) . <400> 7 atg gtt ttc aca cct cag ata ctt gga ctt atg ctt ttt tgg att tca Met Val Phe Thr Pro Gln Ile Leu Gly Leu Met Leu Phe Trp Ile Ser 10 1 15 gcc tcc aga ggt gaa att gtg cta act cag tct cca gcc acc ctg tct Ala Ser Arg Gly Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser 20 gtg tet eea gga gaa aga gee aet ett tee tge agg gee agt eaa aet 144Val Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Thr 35 40 att agc aac aac cta cac tgg tat caa caa aaa cca ggt cag gct cca 192 Ile Ser Asn Asn Leu His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro 50 55 agg ctt ctc atc aag tct gct tcc cag tcc atc tct ggg ata ccc gcc 240 Arg Leu Leu Ile Lys Ser Ala Ser Gln Ser Ile Ser Gly Ile Pro Ala 70 agg ttc agt ggc agt gga tca ggg aca gat ttc act ctc act atc agc 288 Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser 85 90 agt ctg gaa tct gaa gat ttt gca gtg tat tac tgt caa cag agt tac Ser Leu Glu Ser Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Ser Tyr 100 105 381 agt tgg ccg ctc acg ttc ggt caa ggg acc aag gtg gag atc aaa Ser Trp Pro Leu Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys

120

<210> 8

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115

<212> PRT

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<223> Figure 2(B): Light chain variable region of humanized VTm1.1 antibody (HuVTm1.1) .

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Met Val Phe Thr Pro Gln Ile Leu Gly Leu Met Leu Phe Trp Ile Ser $1 \hspace{1.5cm} 5 \hspace{1.5cm} 10 \hspace{1.5cm} 15$

Ala Ser Arg Gly Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser
20 25 30

Val Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Thr
35 40 45

Ile Ser Asn Asn Leu His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro
50 55 60

Arg Leu Leu Ile Lys Ser Ala Ser Gln Ser Ile Ser Gly Ile Pro Ala 65 70 75 80

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser 85 90 95

Ser Leu Glu Ser Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Ser Tyr 100 105 110

Ser Trp Pro Leu Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys 115 120 125

<210> 9

<211> 123

<212> PRT

<213> Homo sapiens

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Glu Val Gln Val Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Lys Tyr
20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val 35 40 45

Ser Gly Ile Ser Ala Ser Gly Glu Asn Thr Tyr Tyr Ala Asp Pro Val 50 55

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Val Tyr 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Asp Asp Thr Ala Met Tyr Tyr Cys
85 90 95

Ala Lys Gly Gly Arg Gln Trp Val Val Leu Gly Tyr Phe Phe Asp Ser 100 105 110

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser

115 120

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1
     5
                    10
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                             25
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
                        40
Tyr Gly Ala Ser Thr Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
                     55
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Asn Ser Leu Gln Ser
                 70
                                    75
Glu Asp Phe Ala Leu Tyr Tyr Cys His Glu Tyr Asn Gly Trp Pro Pro
              85
                                 90
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Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr

105

2

1